

TOWARDS RAPID SCREENING OF TAGGED MR IMAGES OF THE HEART

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Abstract- The final aim of this work is to perform rapid classification of tagged cardiac MR images as normal and abnormal. In the proposed technique, images are first analyzed using harmonic phase analysis and synthetic tags are computed over the myocardium. Cubic curves are fitted to these tags and curve parameters are compared at various regions of the myocardium. In this initial study, the ratios of curve parameters between normal and diseased hearts, such as dilated cardiomyopathy (DCM) and heart with infarcted regions, are evaluated. If the initial segmentation problems are solved, this method could be a very fast and automatic screening tool for identifying diseased locations in tagged MRI.

Keywords - tagged MRI, HARP, cardiac motion

I. INTRODUCTION

MRI tagging means ‘marking’ the myocardium non-invasively. The creation of tags is achieved by the application of specific radio frequency pulses perpendicular to the imaging plane prior to imaging [1]. During the subsequent MR imaging no signal is obtained from the saturated tag tissue and they appear as hypo-intense or black areas. Tags are therefore true non-invasive myocardial markers. Using the motion of the tags, full quantitatively motion estimation of the underlying tissue is possible. This could be very helpful in the diagnosis of cardiac abnormalities. Most of the current available techniques for tag analysis focus only on one of the two successive steps of tag analysis: 1) detecting the tag points, and, 2) developing mathematical myocardial motion models explaining tag motion. HARP analysis, introduced by Nael Osman, combined these two steps and opened the way for rapid functional analysis of the myocardium [2-4]. Our approach uses synthetic tag points found with HARP and tries to differentiate normal and diseased myocardium using their curve parameters.

II. METHODOLOGY

1) *MR Tagging*: The image intensity inside the LV wall can be altered non-invasively with the MR tagging technique [1,5]. Tagged images appear with a spatially encoded pattern that moves with the heart tissue as it moves through the cardiac cycle. The tag pattern creates intensity gradients inside the otherwise homogeneous LV wall, and as a result allows local motion measurement inside the myocardium. The observed motion of a tag provides indirect information about the underlying tissue; it only gives one component of the total past motion from tagging to imaging time. The missing information is filled using the data coming from other tagging directions.

2) *HARP Technique*: By using tagging, energy concentrations occur on the image spectrum (k-space), which HARP technique utilizes. Setting band-pass filters on the first harmonic peak of the spectrum, the first harmonic is isolated and with inverse Fourier transformation a complex HARP image consisting of one amplitude and one phase image data is created. Fig. 1 shows the overview of HARP for a short axis, tagged MR image of a human heart at end-systole. The left ventricle appears as an annulus at the center of the image, and the tag lines, which are straight at end-diastole, are bent due to the heart contraction. The magnitude of the Fourier transform of the original image of Fig. 1a is shown in Fig. 1b. There are five spectral peaks; the one at the center is the DC spectral peak and the other peaks above and below are called the harmonic spectral peaks.

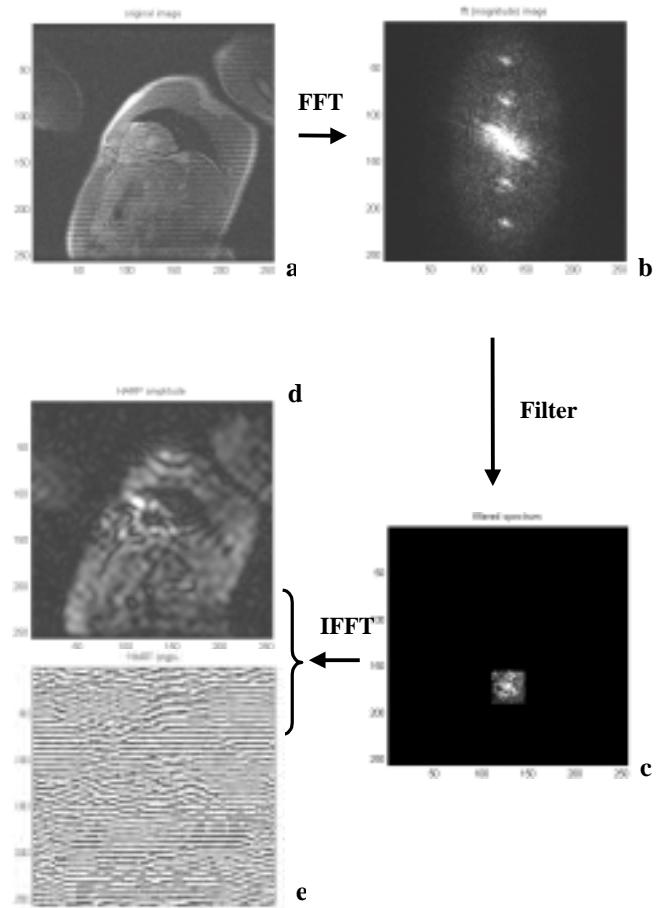


Fig. 1. (a) An LV image with tags. (b) It's Fourier transform showing the magnitude. (c) Filtered spectrum. (d) Magnitude and (e) phase of the complex image

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HARP imaging isolates with a bandpass filter the k^{th} spectral peak centered at frequency ω_k - typically the lowest harmonic frequency in a certain tag direction. The inverse Fourier transform of the bandpass region yields a complex harmonic image (Fig.1.d-e):

$$D_k(y)e^{j\phi_k(y)} = \text{IFFT}\{\text{Filter}\{\text{FFT}[I(x, y)]\}\} \quad (1)$$

where D_k is called the harmonic magnitude image and ϕ_k is called the harmonic phase image. The harmonic magnitude image $D_k(y, t)$ reflects both the changes in geometry of the heart and the image intensity changes caused by tag fading. The motion causes a spreading of the energy around the spectral peak. In short axis images with tag planes parallel to the long axis, the spreading is reasonably localized and it is possible to design a bandpass filter whose band-pass region isolates only a single spectral peak including most of the effects of phase modulation [3].

Our work relies on the determination of the tag points of the human cardiac MR images, and to rapidly ascertain whether the analyzed data is coming from a healthy, or a diseased heart. The initial contour detection of these images is done in Findtags [6]. We continue the analysis by detecting the tag locations, which corresponds to phase discontinuities. We previously had converted the problem of tag localization to zero-crossing detection at each row/column using $\pi/2$ -shifted harmonic phase image [9]. The resulting tag points are fitted to cubic-splines to find out the coefficients for each tag line (l) in every frame (t);

$$F_{l,t}(x) = A_{l,t}x^3 + B_{l,t}x^2 + C_{l,t}x + D_{l,t} \quad (2)$$

where F defines the tag line function with A , B , C and D the cubic curve coefficients. We initially compare the coefficients of a given data set by examining its ratios with other coefficients of known data sets. This examination is performed on 5 healthy, 4 dilated cardio myopathy (DCM), and 5 human infarct tagged MR images.

III. RESULTS

A. Reliability of Tag Detection

We have previously shown the harmonic phase derived tag detection error in synthetic [7] and real, healthy data [9]. The positions of MR tags placed on synthetic images were found with an error of 0.562 ± 0.016 pixel. This was shown to be robust at the expected noise levels. For the tag lines on a healthy human myocardium, the calculated locations were compared to tag points that are found using Findtags. For various frames in the cardiac cycle these errors were: 0.14 ± 0.12 ; 0.18 ± 0.17 ; 0.24 ± 0.22 ; 0.29 ± 0.33 pixel.

The tag points for the end-diastolic and end-systolic frame of a healthy cardiac systole are displayed in Fig. 3. Figures 4

and 5 show the initial analysis for the first tag line of Fig 3. In most cases, the simple cubic polynomial curve-fit is adequate.

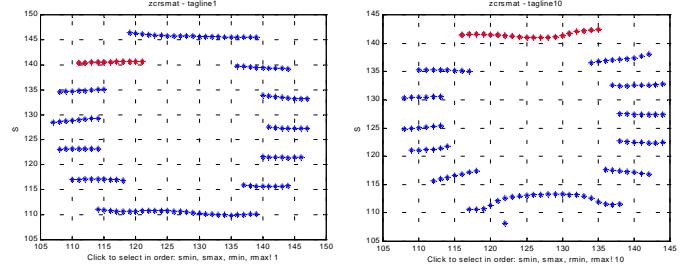


Fig. 3 Calculated tag points for healthy human heart at end-diastole (left) and end-systole (right)

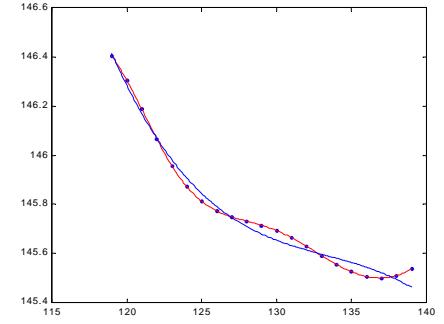


Fig.4 Cubic spline and polynomial data interpolation of the first tag line of tag points represented in Fig.3.

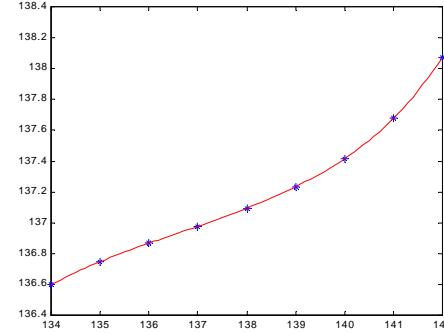


Fig.5 Cubic spline and polynomial data interpolation of the second tag line of the data in Fig.3.

B. Determining Cubic Spline Coefficients for Healthy Data

As mentioned before, the diseased data consists of human dilated (DCM) and infarcted cardiac MR images. The end-systolic tag points for these diseased data are displayed in Fig.6 and 7. In Fig. 8 an example of the curve-fit result is shown, for the tag points of the third tag line from above of the infarcted human cardiac image. The exaggerated curvature is because of zooming on the tag and unequal scaling of both axis.

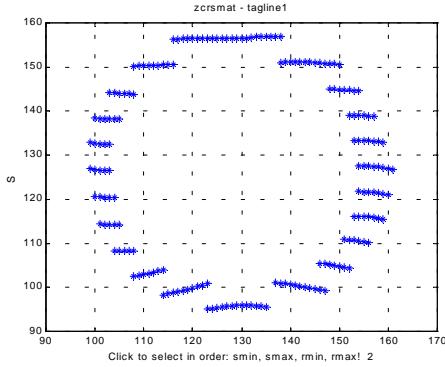


Fig. 6. Calculated tag points of a DCM image

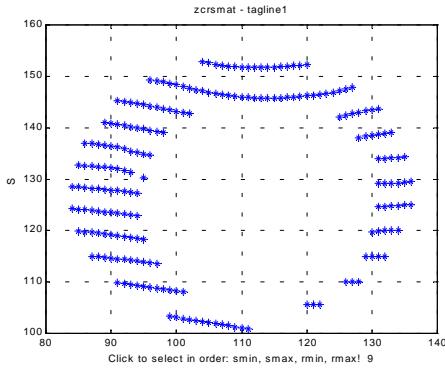


Fig. 7. Determined tag points of an infarct data

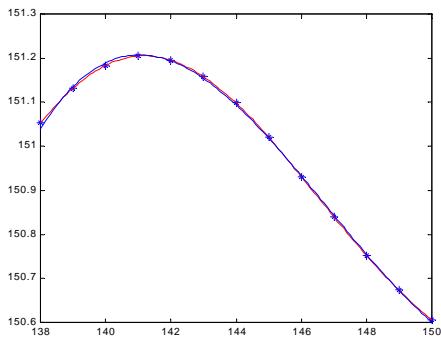


Fig.8 Cubic spline interpolation of the third tag line of tag points represented in Fig.6.

D. Coefficients' Ratios for Normal and Abnormal Data

The curve-fit to the tag line passing through the mid-myocardium at the top portion of the LV for each data set at end-systole is performed to get the coefficients A, B, C and D. Selected coefficients ratios are presented on table 1.

TABLE I
THE RATIO'S FOR THE DCM and INFARCT DATA COEFFICIENTS
(N= Normal, INF=Infarct, DCM=dilated cardiomyopathy)

	A	B	C	D
N1/N2	1.4569	1.5319	1.6056	2.1353
DCM/N1	16.6267	14.1331	12.0454	49.3440
INF/N1	18.9796	31.9010	80.2981	11.5315
DCM/N2	7.6203	6.7689	6.0049	23.4102
INF/N2	8.6987	15.2786	40.0304	5.4709

IV. DISCUSSION

Before analyzing the diseased data coefficients, proportionality between two different healthy human cardiac data is checked. The expectation was that the two data sets should be in similar conditions. The result of this ratio analysis is: 1.4569, 1.5319, 1.6056 and 2.1353. These values are the ratios of the coefficients of first healthy data set and the second.

The proportionality of the coefficients for the healthy data set is performed on the sixth time frame for the first tag line, and their standard deviation is 0.2667. The aim of this selection is that, the motion variation is known, and similar conditions are expected. In fact, in examining the diseased data, the ratios are not in a similar partition. As shown in table I, the coefficients A, B, C and D are different than normal to normal (N1/N2) data comparison. That's expected because as represented in Fig. 6 and 7, the DCM and infarct myocardium differs in systolic motion compared to the healthy myocardium (Fig. 3).

In this work, we had limited number of images on the data set. To deliver an automatic classification for the diseased images, the calculation must be done for many MR tagged cardiac images.

V. CONCLUSION

The aim of this work was to rapidly classify the tagged human cardiac MR images, whether they are normal or abnormal. In our approach, we used the cubic curve fit and we found the polynomial coefficients of the tag line at the end systolic time frame, where the tag displacement is high compared to the first time frame. All of the examined data set of diseased samples differs in the ratio (Table I). The coefficients A, B, C and D are compared for normal to normal (N1/N2), DCM to normal (DCM/N), and infarct to normal (INF/N). These significantly differences between the ratios could lead to classify the data sets. Our future work consists in cluster analysis to identify unknown data sets upon their coefficient variation.

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